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pieces together and if different solutions appear equally plausible. In such a case, one would return to the lab and obtain additional information to resolve the ambiguity. The multi-alignment, or consensus, phase uses more information than just the pairwise alignments in the layout. The sequences of all the fragments in a layout are simultaneously aligned, giving a final set of contigs representing regions of the target genome. An example of an assembly program is PHRAP, which can be found at chimera.biotech.washington.edu/UWGC/tools/phrap.htm.

In the Claims:

Please cancel claims ~~10-15~~ without prejudice to, or disclaimer of the subject matter contained therein.

Please amend the claims as follows:

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1. (Once amended) A substantially purified nucleic acid molecule having a nucleic acid sequence of SEQ ID NO: 1 or complements thereof.

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2. (Twice amended) A substantially purified nucleic acid molecule comprising a fragment nucleic acid having from about 50 to about 100 nucleotide residues; wherein said fragment nucleic acid exhibits complete complementarity to a second nucleic acid molecule having a nucleic acid sequence of SEQ ID NO: 1 or complements thereof.

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6. (Once amended) The substantially purified nucleic acid molecule according to claim 16, wherein said rice protein or fragment thereof is a homologue of a dicot plant protein or fragment thereof.

7. (Once amended) The substantially purified nucleic acid molecule according to claim 16, wherein said rice protein or fragment thereof is a homologue of a non-rice monocot plant protein or fragment thereof.

8. (Once amended) The substantially purified nucleic acid molecule according to claim 16, wherein said rice protein homologue or fragment thereof is a homologue of a non-rice cereal protein or fragment thereof.

9. (Once amended) The substantially purified nucleic acid molecule according to claim 16, wherein said rice protein or fragment thereof is a homologue of a bacterial protein or fragment thereof.

16. (Once amended) A substantially purified nucleic acid molecule encoding a rice protein or fragment thereof from Table 1, wherein said substantially purified nucleic acid molecule comprises a fragment nucleic acid molecule having from about 50 to about 100 nucleotide residues of the nucleic acid molecule of SEQ ID NO: 1.

17. (Once amended) A substantially purified nucleic acid molecule having between 90% and 100% sequence identity with the second nucleic acid molecule of SEQ ID NO: 1 or complements thereof.

Remarks

I. Support for the Amendments

Support for the foregoing claim amendments may be found throughout the specification, and in the original claims. Specifically, support can be found, for example, at page 17, line 22 through page 18, line 4 and at pages 4-9 of the specification as filed. Claims were amended due to Examiner's requirement for election to a single sequence. No new matter was added by way of these amendments.

II. Status of the Claims

By the foregoing amendments, claims 1, 2, 6-9, 16 and 17 have been amended and